

SEQUENCE LISTING

<110> AstaCarotene AB

<120> DNA construct and its use

<130> 29295-AstaCarotene

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2543

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: napin promoter
+ chloroplast localization signal + beta-carotene C-4 oxygenase
coding sequence + termination sequence

<220>

<221> promoter

<222> (1)..(1145)

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<221> transit_peptide

<222> (1179)..(1347)

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<221> CDS

<222> (1179)..(2217)

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<221> terminator

<222> (2273)..(2536)

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tttccaacat tttaaatttc actattggct gaatgcttct tctttgagga agaaacaatt 180

cagatggcag aaatgtatca accaatgcat atatacaaatt gtacctcttg ttctcaaaac 240

atctatcgga tggttccatt tgctttgtca tccaatttagt gactacttta tattattcac 300

tcctctttat tactattttc atgcgagggtt gccatgtaca ttatatttgt aaggattgac 360

gctattgagc gttttcttc aattttcttt attttagaca tgggtatgaa atgtgtgtta 420

gagttgggtt gaatgagata tacgttcaag tgaagtggca taccgttctc gagtaaggat 480

gacctaccca ttcttgagac aaatgttaca ttttagtatac agagtaaaaat gtgtacctat 540

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Met Ala Ser Ser Met
1 5

ctc tct tcc gct act atg gtt gcc tct ccg gct cag gcc act atg gtc 1242
Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala Gln Ala Thr Met Val
10 15 20

gct cct ttc aac gga ctt aag tcc tcc gct gcc ttc cca gcc acc cgc 1290
Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala Phe Pro Ala Thr Arg
25 30 35

aag gct aac aac gac att act tcc atc aca agc aac ggc gga cgc gtt 1338
Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg Val
40 45 50

aac tgc atg tct aga atg cca tcc gag tcg tca gac gca gct cgt cct 1386
Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro
55 60 65

gcg cta aag cac gcc tac aaa cct cca gca tct gac gcc aag ggc atc 1434
Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile
70 75 80 85

acg atg gcg ctg acc atc att ggc acc tgg acc gca gtg ttt tta cac 1482
Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His
90 95 100

gca ata ttt caa atc agg cta ccg aca tcc atg gac cag ctt cac tgg 1530
Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp
105 110 115

ttg cct gtg tcc gaa gcc aca gcc cag ctt tgg ggc gga agc agc agc 1578
Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser
120 125 130

cta ctg cac atc gct gca gtc ttc att gta ctt gag ttc ctg tac act 1626
Leu Leu His Ile Ala Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr
135 140 145

gg tca ttc atc acc aca cat gac gca atg cat ggc acc ata gct ttg Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Leu	1674
150 155 160 165	
agg cac agg cag ctc aat gat ctc ctt ggc aac atc tgc ata tca ctg Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu	1722
170 175 180	
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185 190 195	
cac aac cat act ggc gaa gtg ggg aaa gac cct gac ttc cac aag gga His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly	1818
200 205 210	
aat ccc ggc ctt gtc ccc tgg ttc gcc agc ttc atg tcc agc tac atg Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	1866
215 220 225	
tcc ctg tgg cag ttt gcc cgg ctg gca tgg tgg gca gtg gtg atg caa Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln	1914
230 235 240 245	
atg ctg ggg gcg ccc atg gca aat ctc cta gtc ttc atg gct gca gcc Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	1962
250 255 260	
cca atc ttg tca gca ttc cgc ctc tac ttc ggc act tac ctg cca Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro	2010
265 270 275	
cac aag cct gag cca ggc cct gca gca ggc tct cag gtg atg gcc tgg His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp	2058
280 285 290	
ttc agg gcc aag aca agt gag gca tct gat gtg atg agt ttc ctg aca Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr	2106
295 300 305	
tgc tac cac ttt gac ctg cac tgg gag cac cac aga tgg ccc ttt gcc Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala	2154
310 315 320 325	
ccc tgg tgg cag ctg ccc cac tgc cgc cgc ctg tcc ggg cgt ggc ctg Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu	2202
330 335 340	
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345	
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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: deduced fusion protein of
transit peptide + peptide with beta-carotene C-4 oxygenase activity

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Gln Ala Thr Met Val Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala
20 25 30Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
35 40 45Asn Gly Gly Arg Val Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser
50 55 60Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser
65 70 75 80Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr
85 90 95Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met
100 105 110Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu
115 120 125Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe Ile Val Leu
130 135 140Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His
145 150 155 160Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn
165 170 175Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg
180 185 190Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro
195 200 205Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe
210 215 220Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp
225 230 235 240Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val
245 250 255

Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe
260 265 270

Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser
275 280 285

Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val
290 295 300

Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His
305 310 315 320

Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu
325 330 335

Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
340 345